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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=12; day=22; hr=12; min=50; sec=12; ms=831;
]

=====

Reviewer Comments:

<220>

<221> DOMAIN

<223> CDR3 amino acid sequence of BV14 clonotype derived
from ST specimen of RA patients

<400> 137

Tyr Phe Cs Ala Ser Ser Arg Asp Gly Val Ser Tyr Glu Gln Tyr

1 5 10 15

Phe Gly Pro Gly

Invalid amino acid designator at location (3), Please make necessary
changes.

Application No: 10612468 Version No: 5.0

Input Set:**Output Set:**

Started: 2008-12-09 11:51:59.401
Finished: 2008-12-09 11:52:03.076
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 675 ms
Total Warnings: 116
Total Errors: 55
No. of SeqIDs Defined: 168
Actual SeqID Count: 168

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
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Input Set:

Output Set:

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Actual SeqID Count: 168

Error code	Error Description
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Input Set:

Output Set:

Started: 2008-12-09 11:51:59.401
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Total Errors: 55
No. of SeqIDs Defined: 168
Actual SeqID Count: 168

Error code	Error Description
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E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (110) This error has occurred more than 20 times, will not be displayed
E 323	Invalid/missing amino acid numbering SEQID (137) POS (4)
E 323	Invalid/missing amino acid numbering SEQID (137)at Protein (5)
E 323	Invalid/missing amino acid numbering SEQID (137) POS (9)
E 323	Invalid/missing amino acid numbering SEQID (137)at Protein (10)
E 323	Invalid/missing amino acid numbering SEQID (137) POS (14)
E 331	Count of Protein differs from the <211> tag Input: 19

SEQUENCE LISTING

<110> Zhang, Jingwu Z.
 Ho, Walter Kowk Keung
 Zhang, Dongqing
 Sun, Wei

<120> T Cell Receptor CDR3 Sequence and Methods for
 Detecting and Treating Rheumatoid Arthritis

<130> D6622

<140> 10612468

<141> 2003-07-02

<160> 168

<210> 1

<211> 21

<212> DNA

<213> Artificial Sequence

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<221> CDS

<223> part of the complementary determining region-3 (CDR3)
 in the V(16 family (BV16 gene) of T cell receptors
 (TCR) in patients with rheumatoid arthritis (RA)

<400> 1

agccaagctg acgggaccca t 21

<210> 2

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

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<223> part of the complementary determining region-3
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agttccgggg gcagtcgtgtt c 21

<210> 3

<211> 7

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<223> conserved amino acid sequence derived from CDR3 of
 TCR beta-chain BV16 in patients with RA

<400> 3

Ser Gln Ala Asp Gly Thr His

1 5

<210> 4

<211> 7

<212> PRT

<213> Homo sapiens

<220>

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<400> 4

Ser Ser Gly Gly Ser Leu Phe

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<210> 5

<211> 4

<212> PRT

<213> Homo sapiens

<220>

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<223> amino acid sequence motif derived from CDR3 of TCR
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<400> 5

Ser Trp Gly Gly

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<210> 6

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<223> amino acid sequence of human (beta-chain variable
region V(14 of T cell receptors

<400> 6

Met Gly Pro Gln Leu Leu Gly Tyr Val Val Leu Cys Leu Leu Gly

1 5 10 15

Ala Gly Pro Leu Glu Ala Gln Val Thr Gln Asn Pro Arg Tyr Leu

20 25 30

Ile Thr Val Thr Gly Lys Lys Leu Thr Val Thr Cys Ser Gln Asn

35 40 45

Met Asn His Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Leu

50 55 60

Gly Leu Arg Gln Ile Tyr Tyr Ser Met Asn Val Glu Val Thr Asp

65 70 75

Lys Gly Asp Val Pro Glu Gly Tyr Lys Val Ser Arg Lys Glu Lys

80 85 90

Arg Asn Phe Pro Leu Ile Leu Glu Ser Pro Ser Pro Asn Gln Thr

95 100 105

Ser Leu Tyr Phe Cys Ala Ser Ser

<210> 7
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 <213> Homo sapiens

 <220>
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 1 5 10 15
 Lys Gly Gln Thr Val Thr Leu Arg Cys Asp Pro Ile Ser Gly His
 20 25 30
 Asp Asn Leu Tyr Trp Tyr Arg Arg Val Met Gly Lys Glu Ile Lys
 35 40 45
 Phe Leu Leu His Phe Val Lys Glu Ser Lys Gln Asp Glu Ser Gly
 50 55 60
 Met Pro Asn Asn Arg Phe Leu Ala Glu Arg Thr Gly Gly Thr Tyr
 65 70 75
 Ser Thr Leu Lys Val Gln Pro Ala Glu Leu Glu Asp Ser Gly Val
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 Tyr Phe Cys Ala Ser Ser
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<210> 8
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 PCR analysis

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 PCR analysis

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<210> 10
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<400> 10
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<210> 11
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 <212> DNA
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<220>
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<400> 11
 aggatgggca ctggtcactg t 21

<210> 12
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<400> 12
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<210> 13
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<220>
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 PCR analysis

<400> 13
 ggtgctggcg gactccagaa t 21

<210> 14
 <211> 22
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<220>
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 PCR analysis

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<210> 15
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<212> DNA
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 <220>
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 <210> 16
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 PCR analysis

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 <210> 17
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 <210> 18
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 <220>
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<210> 21
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<210> 22
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<210> 23
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<210> 24
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<210> 25
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<400> 25
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<210> 26
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<220>
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<210> 29
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<212> DNA
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 <220>
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 <210> 30
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 <220>
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 <210> 31
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 <210> 32
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 <220>
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 <210> 33
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 <220>
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<210> 34
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PCR analysis

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<210> 40
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PCR analysis

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<210> 41
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<210> 47
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<210> 48
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<210> 62
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<212> DNA
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<400> 62
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<210> 63
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<210> 64
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<210> 69

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